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OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 06:00:32 ; Search time 681 Seconds
(without alignments)
8770.725 Million cell updates/sec

Title: US-10-617-962-2

Perfect score: 1008
Sequence: 1 atggtttatcaattacacc.....ctcattataaataatgta 1008

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 5394803 seqs, 2962729879 residues

Total number of hits satisfying chosen parameters: 10789606

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

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20: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|--------------------|
| 1 | 1008 | 100.0 | 1008 | 17 | US-10-617-962-2 |
| 2 | 663.8 | 65.9 | 1107 | 17 | US-10-617-962-1 |
| 3 | 663.8 | 65.9 | 1205 | 17 | US-10-617-962-5 |
| 4 | 51 | 5.1 | 8056 | 18 | US-10-473-126-386 |
| 5 | 50.6 | 5.0 | 188971 | 17 | US-10-235-192A-27 |
| 6 | 49.8 | 4.9 | 11394 | 15 | US-10-240-453-95 |
| 7 | 48.8 | 4.8 | 1866 | 16 | US-10-349-680-73 |
| 8 | 48.2 | 4.7 | 2767 | 17 | US-10-301-533-23 |
| 9 | 47.6 | 4.7 | 16217 | 15 | US-10-311-455-597 |
| 10 | 47.4 | 4.7 | 942 | 8 | US-08-781-986A-531 |
| 11 | 47.4 | 4.7 | 942 | 17 | US-10-329-624-531 |

| | | | | | | |
|----|------|-----|---------|----|----------------------|----------------------|
| 12 | 47.4 | 4.7 | 158001 | 17 | US-10-211-193-11 | GENERAL INFORMATION |
| 13 | 47 | 4.7 | 549 | 10 | US-09-991-996-879 | Sequence 879, App |
| 14 | 47 | 4.7 | 11052 | 17 | US-10-257-166-68 | Sequence 68, App |
| 15 | 46.4 | 4.6 | 260 | 17 | US-10-424-559-100851 | Sequence 100851, App |
| 16 | 46.4 | 4.6 | 8056 | 18 | US-10-473-126-240 | Sequence 240, App |
| 17 | 46.2 | 4.6 | 34722 | 18 | US-10-322-281-700 | Sequence 700, App |
| 18 | 46 | 4.6 | 32392 | 19 | US-10-706-635-27 | Sequence 27, App |
| 19 | 45.6 | 4.5 | 18283 | 17 | US-10-221-613-326 | Sequence 326, App |
| 20 | 45.4 | 4.5 | 225070 | 13 | US-10-087-192-1990 | Sequence 1990, App |
| 21 | 45.2 | 4.5 | 4985 | 14 | US-10-094-240-10 | Sequence 10, App |
| 22 | 45.2 | 4.5 | 4985 | 16 | US-10-056-405-10 | Sequence 10, App |
| 23 | 45.2 | 4.5 | 13377 | 17 | US-10-311-455-1436 | Sequence 1436, App |
| 24 | 45.2 | 4.5 | 13377 | 17 | US-10-221-714A-198 | Sequence 198, App |
| 25 | 45 | 4.5 | 6103 | 15 | US-10-311-455-1664 | Sequence 1664, App |
| 26 | 44.8 | 4.4 | 1046 | 13 | US-10-027-632-10421 | Sequence 10421, App |
| 27 | 44.8 | 4.4 | 1046 | 17 | US-10-027-632-10421 | Sequence 10421, App |
| 28 | 44.8 | 4.4 | 3399 | 18 | US-10-793-639-600 | Sequence 600, App |
| 29 | 44.6 | 4.4 | 973 | 17 | US-10-424-539-58879 | Sequence 58879, App |
| 30 | 44.6 | 4.4 | 1488 | 9 | US-09-815-242-4589 | Sequence 4589, App |
| 31 | 44.6 | 4.4 | 1491 | 9 | US-09-815-242-8559 | Sequence 8559, App |
| 32 | 44.6 | 4.4 | 1491 | 9 | US-10-282-132A-8174 | Sequence 8174, App |
| 33 | 44.6 | 4.4 | 13508 | 8 | US-08-781-9864-120 | Sequence 120, App |
| 34 | 44.6 | 4.4 | 13508 | 17 | US-10-329-624-120 | Sequence 120, App |
| 35 | 44.6 | 4.4 | 3673778 | 16 | US-10-312-841-1 | Sequence 1, App |
| 36 | 44 | 4.4 | 609 | 17 | US-10-424-539-102915 | Sequence 102915, App |
| 37 | 44 | 4.4 | 831 | 19 | US-10-706-635-69 | Sequence 69, App |
| 38 | 44 | 4.4 | 18683 | 15 | US-10-311-455-285 | Sequence 285, App |
| 39 | 44 | 4.4 | 18683 | 16 | US-10-240-452-33 | Sequence 33, App |
| 40 | 44 | 4.4 | 50000 | 19 | US-10-706-635-24 | Sequence 24, App |
| 41 | 44 | 4.4 | 3673778 | 16 | US-10-312-841-2 | Sequence 2, App |
| 42 | 43.8 | 4.3 | 54775 | 18 | US-10-741-601-5659 | Sequence 5659, App |
| 43 | 43.8 | 4.3 | 54775 | 19 | US-10-741-600-17684 | Sequence 17684, App |
| 44 | 43.8 | 4.3 | 3673778 | 16 | US-10-312-841-1 | Sequence 1, App |
| 45 | 43.6 | 4.3 | 6418 | 15 | US-10-311-455-286 | Sequence 286, App |

ALIGNMENTS

RESULT 1
US-10-617-962-2
; Sequence 2, App
; Publication No. US20040055036A1
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Research Organisation
; APPLICANT: EAST, Peter David
; TITLE OF INVENTION: Toxin Genes from the Bacteria Xenorhabdus nematophilus and Photob
; FILE REFERENCE: 050179-0076
; CURRENT APPLICATION NUMBER: US/10/617,962
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US/09/463,048A
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PCT/AU98/00562
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: PO 8088
; PRIOR FILING DATE: 1997-07-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1008
; TYPE: DNA
; ORGANISM: Photorhabdus luminescens
US-10-617-962-2

Query Match 100.0%; Score 1008; DB 17; Length 1008;
Best Local Similarity 100.0%; Pred. No. 1.9e-198;
Matches 1008; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTTATCAATTAAACCCGATGATGAAGTGAATATCCACCCGTTGAAACCAATA 60
Db 1 ATGTTATCAATTAAACCCGATGATGAAGTGAATATCCACCCGTTGAAACCAATA 60

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QY 61 GCAGAGATATAGTACTGATCTAACTTTAAGCAACAGATGAGGTCATACAGATCA 120
DB 61 GCAGAGATATAGTACTGATCTAACTTTAAGCAACAGATGAGGTCATACAGATCA 120
QY 121 TATGAAATGAAATGAGCTAAGAAATTAATTAGCTTACGCTTTGGCTGTAAGTGT 180
DB 121 TATGAAATGAAATGAGCTAAGAAATTAATTAGCTTACGCTTTGGCTGTAAGTGT 180
QY 181 ATTCAATATGATCTAACTTCTGATGACTATTTATAGATAAAGAGACTGCTGAGAG 240
DB 181 ATTCAATATGATCTAACTTCTGATGACTATTTATAGATAAAGAGACTGCTGAGAG 240
QY 241 ATTATCAAGATATATGCTTAATCTTCACTGCACTATAGGTGAAATGGTATCA 300
DB 241 ATTATCAAGATATATGCTTAATCTTCACTGCACTATAGGTGAAATGGTATCA 300
QY 301 ATTTCTAAAGATATGAGCAATGGTTTTTAAAGAAATGGAATTTTGAAGGTCAATAT 360
DB 301 ATTTCTAAAGATATGAGCAATGGTTTTTAAAGAAATGGAATTTTGAAGGTCAATAT 360
QY 361 CCTCAAAACATTTGGAATGTTCTGAGCTTGAATAATTAACCATGAGTGTATTGAGAT 420
DB 361 CCTCAAAACATTTGGAATGTTCTGAGCTTGAATAATTAACCATGAGTGTATTGAGAT 420
QY 421 GACGATAAATTTATGACCTATATTTTTTCTGTAACAGAAATTCACATGAGAAAT 480
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QY 481 CAACATCAATGCGGCAAGATTTTAAATTAATGATTTCTTATTTACCTTATCTGCT 540
DB 481 CAACATCAATGCGGCAAGATTTTAAATTAATGATTTCTTATTTACCTTATCTGCT 540
QY 541 GTAACCTCACTGGGAGAGATTTTTCAAAAAATTTTCAATGATTTAGAGGCTAA 600
DB 541 GTAACCTCACTGGGAGAGATTTTTCAAAAAATTTTCAATGATTTAGAGGCTAA 600
QY 601 TCAATTAGAAATTAATGAGAAAAAAATCTTTCTAAACCTTTCTTGAACACGCGAG 660
DB 601 TCAATTAGAAATTAATGAGAAAAAAATCTTTCTAAACCTTTCTTGAACACGCGAG 660
QY 661 AGATTTCCTGATGCGAATAGTTATTTGGCTGACCAACAGAGCGCTTAATGAGAG 720
DB 661 AGATTTCCTGATGCGAATAGTTATTTGGCTGACCAACAGAGCGCTTAATGAGAG 720
QY 721 GTGAGTTTAAAGAACTTAAATAATCAATCTAGGAATGATTTCTAATATGAAAGG 780
DB 721 GTGAGTTTAAAGAACTTAAATAATCAATCTAGGAATGATTTCTAATATGAAAGG 780
QY 781 GCTGCAAAACAAAGATATGCTTATTAATAAAGAGTACAAAGGTTAAGCTCCAG 840
DB 781 GCTGCAAAACAAAGATATGCTTATTAATAAAGAGTACAAAGGTTAAGCTCCAG 840
QY 841 AAGAGCGCAAAAGTATTTGTTACAGCAGTGGAGTAACTGAAAAATTTGCCGATAT 900
DB 841 AAGAGCGCAAAAGTATTTGTTACAGCAGTGGAGTAACTGAAAAATTTGCCGATAT 900
QY 901 TTAATAGTGTAGGCTAAGCCAAAAAGCAGGGTAACTTTAAGCAATGATATGAC 960
DB 901 TTAATAGTGTAGGCTAAGCCAAAAAGCAGGGTAACTTTAAGCAATGATATGAC 960
QY 961 AATACAAATGACGGTTCATAGTGTGGAACCTTATTAATAATATATGA 1008
DB 961 AATACAAATGACGGTTCATAGTGTGGAACCTTATTAATAATATATGA 1008

RESULT 2
US-10-617-962-1
; Sequence 1, Application US/10617962
; Publication No. US20040055036A1
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Research Organisation
; APPLICANT: EAST, Peter David
; TITLE OF INVENTION: Toxin Genes from the Bacteria Xenorhabdus nematophilus and Phoxo
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; TITLE OF INVENTION: luminescens
; FILE REFERENCE: 050179-0076
; CURRENT APPLICATION NUMBER: US/10/617,962
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US/09/463,048A
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PCT/AU98/00562
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: PO 8088
; PRIOR FILING DATE: 1997-07-17
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Xenorhabdus nematophilus
US-10-617-962-1

Query Match 65.9%; Score 663.8; DB 17; Length 1107;
Best Local Similarity 79.4%; Pred. No. 2,7e-127;
Matches 835; Conservative 0; Mismatches 162; Indels 54; Gaps 2;

QY 12 ATTAACACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 71
DB 57 AGTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 116
QY 72 AGTAAAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 131
DB 117 ATATGAGTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 176
QY 132 ATATGAGTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 191
DB 177 ATATGAGTACTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 236
QY 192 ATCTAACTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 251
DB 237 CTCTCACTTCCAGAACTATTAATAATTAAGATTAACAAGCTAGATTTATCAAGA 296
QY 252 ATATATGCTATCTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 311
DB 297 ATATATGCTATCTTATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 356
QY 312 TATGCAATATGATTTTAAAGTAACTGATGATGATGATGATGATGATGATGATGATGAT 371
DB 357 TATGCAATATGATTTTAAAGTAACTGATGATGATGATGATGATGATGATGATGATGAT 416
QY 372 TTAGATGTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 431
DB 417 CTGGAATATTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 476
QY 432 ATTACACATATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 491
DB 477 ATTACACATATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 536
QY 492 TCCCAAGATTTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 551
DB 537 TGCAGCAATTTTAAAGTAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 596
QY 552 GGAAGAGAGATTTTCAAAAACTTTTACAGTATGAGTAAATCAATCAATCAATCAATCAAT 611
DB 597 GGAAGAGAGATTTTCAAAAACTTTTACAGTATGAGTAAATCAATCAATCAATCAATCAAT 656
QY 612 TTAATTTAGAGAAAAAATTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTT 671
DB 657 TTAATTTAGAGAAAAAATTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTTTCAAAAACTTT 716
QY 672 TGCAGCAATTTTAAAGTAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 714
DB 717 TGCAGCAATTTTAAAGTAACTGATGATGATGATGATGATGATGATGATGATGATGATGAT 776
QY 715 -----TGAAGTGAAGTTTAAAGACTTAA 740
DB 777 TACAGCAACAGCTTACAGCAGCTTCAATCAATGAGAGATGATGATGATGATGATGATGATGAT 836
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Best Local Similarity 45.3%; Pred. No. 2.6;
Matches 226; Conservative 0; Mismatches 270; Indels 3; Gaps 1;

QY 141 TAGAAAAATTAATTTAGCTTACGCTTGCTGTAAGTGGTAATTCATAATGTAATCTAACT 200
DB 1365 TAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1306
QY 201 TCCGTGAGCTATTATAGAAATTAAGAGCTGCTGAGAGAAATTTATCAAGAAATATATGTC 260
DB 1305 ATTAATTTTAAAAAATATTAATTTTATTAATTAATTAATTAATTAATTAATTAATTTT 1246
QY 261 TAATCTTTCATCTGCACTATAGGTAAGTAATGCTGTAATTCCTCAAAATTTGGAATG 320
DB 1245 TATTCAAAAAATTAATTTATTAATTAATTAATTAATTAATTAATTAATTAATTTAA 1186
QY 321 TGGTTTAAAGAAATGAACTGATTTTGAAGTCAATATCCCAAAATTTGGAATG 380
DB 1185 ATAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1126
QY 381 TCCGTGAGCTGAAATTAACATTAAGTCTTATTCAGATGAGATTAATTAATTAATTAAT 440
DB 1125 TAAAAAAGCAATATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1069
QY 441 ATATTTTCTCTGTAAGGAAATTCCTGAGGAAATCAAAATCAAAATGCGCAAG 500
DB 1068 TTTTATTTATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1009
QY 501 ATTTTAAATTAATTAATTAATTTCTTATTTACCTTATGCTGTAATTCCTGGAAGAG 560
DB 1008 AATTAATTTTAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 949
QY 561 GATTTTTCAAAAAATTTTACATGATGATTAAGGCTTAATCAATTAATTAATTAATTAAT 620
DB 948 TATTTTAAAAAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 889
QY 621 GAGAAAAAATCTTTCTTAA 639
DB 888 ATTAACAAAAATTTTATATCA 870

RESULT 5

US-10-235-192A-27
; Sequence 27, Application US/10235192A
; Publication No. US2004004389A1
; GENERAL INFORMATION:
; APPLICANT: McCarthy, Jeanette
; TITLE OF INVENTION: Methods and Compositions for Identifying
; TITLE OF INVENTION: Risk Factors for Abnormal Lipid Levels and the Diseases
; FILE REFERENCE: MMI-011
; CURRENT APPLICATION NUMBER: US/10/235,192A
; CURRENT FILING DATE: 2002-09-04
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 27
; LENGTH: 188971
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 145329-145428, 187896-187995, 195894-195993
; OTHER INFORMATION: N = any nucleotide
US-10-235-192A-27

Query Match 5.0%; Score 50.6; DB 17; Length 188971;
Best Local Similarity 42.6%; Pred. No. 10;
Matches 263; Conservative 0; Mismatches 354; Indels 0; Gaps 0;

QY 12 ATTAACACCTGATGATGAGATATCCACCGTTGAAAAGCAATATGACGAGATAT 71
DB 103629 ATCTATATATGAT 103688
QY 72 AGTAGCTATATTAACCTTTAAGCAACAGATGAGGCTCATACGATCATATGGAATTGA 131

DB 103689 ATGAATATCTATATGAATATCTATATATGAATATCTATGAATATCTATATATGAATATCT 103748

QY 132 ATATGAGCTAAGAAAAATTAATTTAGCTTACGCTTGGCTGTAAGTGGTAATTCATAATGCT 191

DB 103749 ATATGAATATATGATGAATATATGAATATATATGAATATATGAATATATGAATATAT 103808

QY 192 ATCTAACTTCCCTGAGCTATTATTAAGAAATTAAGAGCTGCTGAGAGAAATTTATCAAGA 251

DB 103809 ATGAATATCTATGAATATCTATATGAATATATATGAATATCTATATGAATATATATATG 103868

QY 252 ATATATGCTTAATCTTTCATCTGCACTATTAAGTGAATGTAATGTAATGTAATGTAATGTAAT 311

DB 103869 AATTAATATGAATTTATATATATGAATATATATGAATATATATGAATATATATATATGA 103928

QY 312 TATGCAAAATGTTTATTAAGAAATGAACCTGATTTTGAAGTCAATATCCCAAAATCAT 371

DB 103929 TATATATATGAATATATATATGAATATATATGAATATATATGAATATATATATATGA 103988

QY 372 TTGAATGTCCTGAGCTTGAATAAATTAACATTAAGTGTCTTATTCAGATGAGATTAAT 431

DB 103989 TATATATGAATATATATATGAATATATATGAATATATATGAATATATATATATATAT 104048

QY 432 ATTAACACTATATTTTCTCTGTAAGGAAATTCCTGAGGAAATTCAGAGAAATCAAAATCA 491

DB 104049 TATATGAATATATATATGAATATATATGAATATATATGAATATATATATATATATAT 104108

QY 492 TGCCCAAGATTTTAAATTAATTAATGATTTCTATATTAATCTTATGCTGTAATCTACT 551

DB 104109 TGAATTAATTAATGAATATATATGAATATATATGAATATATATGAATATATATATATGA 104168

QY 552 GGAAGAGAGATTTTTCAAAAAATTTTACATGATGATTAAGGCTTAATCAATTAATTAAGAA 611

DB 104169 ATTAATATATGAATATATATATGAATATATATGAATATATATGAATATATATATATGA 104228

QY 612 TTAATTTGAGAGAAAA 628

DB 104229 ATATATGAATATATATAT 104245

RESULT 6

US-10-240-453-95
; Sequence 95, Application US/10240453
; Publication No. US20030148326A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIPENBROCK, Christian
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
; TITLE OF INVENTION: Transcription
; TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated
; FILE REFERENCE: 5013.1009
; CURRENT APPLICATION NUMBER: US/10/240,453
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03973
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019056.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 95
; LENGTH: 11394
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-453-95

| | Query Match | Similarity | 4.8% | Score 48.8 | DB 16 | Length 1866 |
|----|-------------|--|-------|----------------|----------------|-------------|
| | Best Local | Similarity | 47.3% | Pred. No. 4.4 | Mismatches 267 | Indels 10 |
| | Matches | Conservative | 0 | Mismatches 267 | Indels 10 | Gaps 3 |
| QY | 122 | ATGGAATTGAATTATGAGCTTAAGAAAATAATATATAGCTTAAGCTTTGGCTGTAAGTGTGA | 181 | | | |
| Db | 1037 | ATGAAAAAACAACAAATTAAGATTATTTAGATCTTTTGATTAAGATTGAATTAAT | 1096 | | | |
| QY | 182 | TTCAATTAATGTAATCTTAACCTCTGTACTTTATTAAGATTAAGACCTGCTAGAGA | 240 | | | |
| Db | 1097 | TTCAAAAATTAATTCATATAATTTAGATTAATTAATTAATTAATTTCAAAAGGAGCAT | 1156 | | | |
| QY | 241 | --ATTATCAAGATATATATGCTTAATCTTCACTGCACTATTAGTGAAAATGCTGATC | 298 | | | |
| Db | 1157 | ATATTACACAAAAAATAATTAATAAAATCTTTATTTAGATGCTTCAATTAATATGATGCTC | 1216 | | | |
| QY | 299 | AAATTTCAAAAGATATGCAAAATGATTTTATTAAGAAATGCACTGGAATTTGAAGGCAAT | 358 | | | |
| Db | 1217 | AAATTACAAATATCTTAATTCACAAAATGATTAAGAAATACCAAAATTAATTAATTAATAC | 1278 | | | |
| QY | 359 | ATCTCAAAACATTTGGAATGTTCTCTGAGCTTGAATAATTAACATTAAGTCTTAATTCAG | 418 | | | |

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Query Match          4.8%; Score 48.2; DB 17; Length 2767;
Best Local Similarity 56.7%; Pred. No. 6.7;
Matches 89; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

QY      243  TTATCAAGAAATATATGTCATATCTTTTCATCTGCATATTAGGTGAAAAATGGTGATCAAT 302
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      562  TGATCTGATATAAAATTTCTCTGTTTCCTCAATTACATTTAGATGAAAAAATGACAAAT 621

QY      303  TTCTAAAGATATGGCAAAATGGTTTTTATATAGATGAAGACTGCATTTTGAAGTCAATATCC 362
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      622  GTGTAAATGAAGATGAGGATCATTTTTTAAATAAATAAATATTTAAAGATATGATGC 681

QY      363  TCAAAACATTTGGAATGTTCCTGAGCTTGAATAATAA 399
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB      682  TGATGAAGTATACATATATATATGATGATCACTATAAA 718

RESULT 9
US-10-311-455-597
; Sequence 597 Application US/10311455
; Publication No. US20030143606A1
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with the Immune System by Deter
; TITLE OF INVENTION: cytosine methylation
; FILE REFERENCE: 5013.1014
; CURRENT APPLICATION NUMBER: US/10/311,455

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;; CURRENT FILING DATE: 2002-12-16
;; PRIOR APPLICATION NUMBER: PCT/EP01/07537
;; PRIOR FILING DATE: 2001-07-02
;; PRIOR APPLICATION NUMBER: DE 10032529.7
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: DE 10043826.1
;; PRIOR FILING DATE: 2000-09-01
;; NUMBER OF SEQ ID NOS: 2424
;; SEQ ID NO 597
;; LENGTH: 16217
;; TYPE: DNA
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
;; FEATURE:
;; NAME/KEY: unsure
;; LOCATION: 12269
;; OTHER INFORMATION: n is a or g or c or t
US-10-311-455-597

Query Match 4.7%; Score 47.6; DB 15; Length 16217;
Best Local Similarity 43.3%; Pred. No. 17; Mismatches 289; Indels 0; Gaps 0;
Matches 221; Conservative 0;

QY 124 GGAATTGAATATCGAGCTAAGAAAATATATAGCTTACGCTTGGCTGAAGTGTATT 183
DB 2495 GAAATATATATTTTATATATAAAATATGAATAATGTAATATATAAGATGTAATG 2554
QY 184 CATTAATGATCTAAACTTCTGATGACTTTATAGAAATAAAGAGCTGCTGAGAAATT 243
DB 2555 AAGAAAAATTAATAAT 2614
QY 244 TATCAAGATATATATGCTATCTTCATCTGCACATTTAGTGAANAATGCTATCAATT 303
DB 2615 TGGGGTTTGTATGTTAT 2674
QY 304 TCTAAGATATGCAAAATGTTTATATAGAAATGAATCTGATTTGAAAGTCAATATCT 363
DB 2675 TATATATATATGATTAATATATATATATATATATATATATATATATATATATAT 2734
QY 364 CAAACATTTGGATGTTCTCGAGCTTGAAAATAAACATGAGTCTTATTCAGATGAC 423
DB 2735 AAGATATATTAATATATGTTGATATGATTTATATATATATATATATATATATAT 2794
QY 424 GATTAATATTTAGCATATATATTTTCTGTAACAGAAATCCATGAGAAATCA 483
DB 2795 AGTATTTAGTTAGATTTATATATATATATATATATATATATATATATATATAT 2854
QY 484 CAATCAATGCGCAGATTTTATATATATATATATATATATATATATATATATATAT 543
DB 2855 TTTTATATATGAAAAAGATTTTGTGTTGTAGTTTATATATATATATATATATAT 2914
QY 544 ACTTCACTGGAGAGAGATTTTTCAAAAAATTTTAACANGATTTAGAGCTAAATCA 603
DB 2915 AGTAGTAGTTTATTTTGTATTTAGTTAAAAAGTATATAATATATATATATATAT 2974
QY 604 TTAGAGATTTATTTGAGAGAAAAAACT 633
DB 2975 AGTGGAAATTTATAGAGAAATTTAAATTT 3004

RESULT 10
US-08-781-986A-531
; Sequence 531, Application US/08781986A
; Publication No. US20030054436A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville

;; STATE: Maryland
;; COUNTRY: USA
;; ZIP: 20850
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
;; COMPUTER: HP Vectra 486/33
;; OPERATING SYSTEM: MSDOS version 6.2
;; SOFTWARE: ASCII Text
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/781,986A
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER:
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Benson, Bob
;; REGISTRATION NUMBER: 30,446
;; REFERENCE/DOCKET NUMBER: PB248BP
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (301) 309-8504
;; TELEFAX: (301) 309-8512
;; INFORMATION FOR SEQ ID NO: 531:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 942 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
US-08-781-986A-531

Query Match 4.7%; Score 47.4; DB 8; Length 942;
Best Local Similarity 47.8%; Pred. No. 6; Indels 0; Gaps 0;
Matches 138; Conservative 0; Mismatches 151; Indels 0; Gaps 0;

QY 66 AGATATAGTACTATATCTTAACCTTTAAGCAACAGATGAGGCTCTACGATCATATAG 125
DB 313 AAAAAACGACTTAATCTACGCAAAATGACCAATTAGATGACAGATTAAGTCACTTCTAT 372
QY 126 AATTAATATGAGTGAAGAAATATATATTTAGCTTACGCTTGGCTGATAGTATCA 185
DB 373 AGATGAATATTAAGGCTCTAATCTGATTCGTATATGATGATGATGATGATGATGATG 432
QY 186 TAATGATATCTAACTCTCGATGACTATATATTAAGATTAAGAGACTGCTGAGAAATTTA 245
DB 433 CATAGAGAGAAAT 492
QY 246 TCAAGATATATGCTTAATCTTCAATCTGCACTATATAGTGAAAAATGGTCAATTTTC 305
DB 493 AACGCCATCAATGCTGATTTTGTATTTTATATATATATATATATATATATATATAT 552
QY 306 TAAAGATATGCAATGTTTATATAGAAATGAATCTGATTTTGAAGGT 354
DB 553 AAAACAGAGACATACGCTTTATTAAGAAAGAAATTTCTATTAAGAT 601

RESULT 11
US-10-329-624-531
; Sequence 531, Application US/10329624
; Publication No. US20040043037A1
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gail H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland

| Matches | 410 | Conservative | 0 | Mismatches | 536 | Indels | 11 | Gaps | 3 |
|---------|--------|--|---|------------|-----|--------|----|------|--------|
| QY | 57 | AATAGCGAGATATAGTACGTATATCTAACTTTAAGCAACAGATGAGCGTCATACAC | | | | | | | 116 |
| Db | 126950 | AAT | | | | | | | 127009 |
| QY | 117 | ATCATATATGAAATGAAATAT-----CGAGCTAAGAAAATATATATAGCTTAACGTTGGCTG | | | | | | | 172 |
| Db | 127010 | ATAAT | | | | | | | 127069 |
| QY | 173 | TAAAGGTATTCATATATATGATCTTCAAACTTCCTGATGACTATATATATATATATATATAT | | | | | | | 232 |
| Db | 127070 | TAAAAAAT | | | | | | | 127129 |
| QY | 233 | CTGAGAGAAATTTATCAAGATATATATGCTAATCTTTCAATCTGCACTATATAGTGAAATG | | | | | | | 292 |
| Db | 127130 | TAT | | | | | | | 127189 |
| QY | 293 | GTGATCAAAATTTCTTAAAGATATATGCAATGCTTTTATATAGAAATGACATCGAATTTTGAAG | | | | | | | 352 |
| Db | 127190 | AT | | | | | | | 127249 |
| QY | 353 | GTCAATATCTCAAAAACATTTGGAATGTCTCGAGCTTGAAATATTAACCATGAGTCTT | | | | | | | 412 |
| Db | 127250 | ATAAT | | | | | | | 127309 |
| QY | 413 | ATTGAGATGACGATTAAT | | | | | | | 466 |
| Db | 127310 | TTAT | | | | | | | 127369 |
| QY | 467 | CACGAGAGAAATATCAACATCAAAATGCCCAAGTTTTTAAATTAATGATTTCTTAT | | | | | | | 526 |
| Db | 127370 | TAT | | | | | | | 127429 |
| QY | 527 | TTACCTTATCTGCTGTAACCTTCACTGGAGAGAGATTTTTTCAAAAACTTTTACAAATG | | | | | | | 586 |
| Db | 127430 | AT | | | | | | | 127489 |
| QY | 587 | GATTAGAGGCTTAATCATTTAGAGATTAATTTAGAGAAAAAAACCTTTCTAACCCTTCT | | | | | | | 646 |
| Db | 127490 | TAT | | | | | | | 127548 |
| QY | 647 | TTGCAACACCGCAGAGATTACCTGATGCGAGATATGTTATTTGGCTGCAACAAGAAG | | | | | | | 706 |
| Db | 127549 | AT | | | | | | | 127608 |
| QY | 707 | CGCCTAATGAGAGTGAAGTTTAAAGAACTTAAATATATCAAAATCTAGATGAGTTT | | | | | | | 766 |
| Db | 127609 | AT | | | | | | | 127668 |
| QY | 767 | CTAATATATGAGGGGCTGCAAAAACAAAGTATATGTTCAATTTTAAAGAGTACAAAGG | | | | | | | 826 |
| Db | 127669 | AT | | | | | | | 127728 |
| QY | 827 | GTAACGCTCCACAGACAGACAGCAAGAAAGTATTTGTACAGCCAGTGGCACTAACC | | | | | | | 886 |
| Db | 127729 | TAAAT | | | | | | | 127788 |
| QY | 887 | AATTCGCCAAT | | | | | | | 946 |
| Db | 127789 | AT | | | | | | | 127848 |
| QY | 947 | AAATATGATCTGACAAATCAATGACGTTCACTATAGTTGGAACCTATTTAAAAATA | | | | | | | 1003 |
| Db | 127849 | AT | | | | | | | 127905 |

RESULT 13

US-09-991-936-879/c

Sequence 879, Application US/09991936

Publication No. US20030073827A1

GENERAL INFORMATION:

APPLICANT: Brandt, Kevin S.

```
/ APPLICANT: Gaines, Patrick J.
/ APPLICANT: Stinchcomb, Dan T.
/ APPLICANT: Wisniewski, Nancy
/ TITLE OF INVENTION: FLUA HEAD, NERVE CORD, HINDGUT AND MALPIGHIAN TUBULE
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES, PROTEINS AND USES THEREOF
/ FILE REFERENCE: PC-6-CI
/ CURRENT APPLICATION NUMBER: US/09/991,936
/ CURRENT FILING DATE: 2001-11-21
/ PRIOR APPLICATION NUMBER: US/09/543,668
/ PRIOR FILING DATE: 2000-04-07
/ PRIOR APPLICATION NUMBER: 60/128,704
/ PRIOR FILING DATE: 1999-04-09
/ NUMBER OF SEQ ID NOS: 1959
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 879
/ LENGTH: 549
/ TYPE: DNA
/ ORGANISM: Ctenocephalides felis
US-09-991-936-879
```

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Query Match          4.7%; Score 47; DB 10; Length 549;
Best Local Similarity 49.0%; Pred. No. 6.6;
Matches 125; Conservative 0; Mismatches 130; Indels 0; Gaps 0;
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QY 372 TTGGAATGTTCCGAGCTGAAATTAACCATGAGTCTTATTCAGATGAGTAAT 431
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 335 TTTTATAGCTTTAAAGTTTACTTTTAAATAATGCTTTTGCAATATGAGATATGA 276
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 432 ATTGACATATATTTTCTCTGTCAGAGAAATTCACCTGAGAGAAATCAATCAAA 491
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 275 TCTAAGACACATTTCTTTTTCATGCAAAATTCATCATATTTTAAAGCTTCAT 216
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 492 TCCCGCAATTTTAAATTAATGATTTCTTATTTACTTCTGCTGTAATTCAC 551
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 215 TTCCATACCATTTATGATTTGTCAGATTAATGGAACCTTACTTTTCAATGAGTT 156
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 552 GGAAGAGAGATTTTTCAAAAAATTTTACATGATGAGGCTTAATCAATGAGAA 611
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 155 TAGACTAATTAATTTAATTTAATGTTGACTTCAATTAAGCGAAATTAATTTTATA 96
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 612 TTATATTTGAGAGAA 626
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 95 TCAGTGTGTAATGAAA 81
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 14
US-10-257-166-68
/ Sequence 68, Application US/10257166
/ Publication No. US20040023230A1
/ GENERAL INFORMATION:
/ APPLICANT: OLEK, Alexander
/ APPLICANT: PIERENBERG, Christian
/ APPLICANT: BERLIN, Kurt
/ TITLE OF INVENTION: Method and Nucleic Acids for Analysing the Methylation of
/ FILE REFERENCE: 5013.1011
/ CURRENT APPLICATION NUMBER: US/10/257,166
/ CURRENT FILING DATE: 2002-10-07
/ PRIOR APPLICATION NUMBER: PCT/EP01/07470
/ DE 10032529.7
/ DE 10043826.1
/ PRIOR FILING DATE: 2001-06-29
/ 2000-06-30
/ 2000-09-01
/ NUMBER OF SEQ ID NOS: 178
/ SEQ ID NO 68
/ LENGTH: 11052
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-257-166-68
```

```
Query Match          4.7%; Score 47; DB 17; Length 11052;
Best Local Similarity 48.7%; Pred. No. 20;
Matches 128; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

QY 225 AGAGCTGCTGAGAGAAATTTATCAAGATATATGCTAATCTTATCTGACCTTTAGG 284
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1196 AGAAAGTATGATGATATTTTAAAGTTTGGGTTTTTTTAAAGATATATATATGG 1255
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 285 TGAATATGATGATCAATTTCTTAAAGATATGCAATGTTTATTAAGAAATGAATGGA 344
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1256 AGTAAATGTTTAAAGATGAGAAAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1315
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 345 TTTTGAAGTCAATATCTCAAAACATTTGGAATGTTCTGAGCTTGAATTAACCAAT 404
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1316 TTTATAGTATTTTATTAATAAGGGGTTTGGGTGAAGGTATTAATAATAAGTTT 1375
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 405 GAGTCTTATTCAGATGACGATTAATTTTACACTATATTTTCTCTGTCAGAGAAAT 464
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1376 AAAAATTAATAATTTTGTATTTTATGTTATTTTGTATTTTGTATTTATAGATTA 1435
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 465 TCCACTGAGGAAATCAACAAT 487
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1436 TTGAGTTTGTAAATTTATAGT 1458
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 15
US-10-424-599-100851
/ Sequence 100851, Application US/10424599
/ Publication No. US20040031072A1
/ GENERAL INFORMATION:
/ APPLICANT: La Rosa Thomas J
/ APPLICANT: Kovalic David K
/ APPLICANT: Zhou Yihua
/ APPLICANT: Cao Yongwei
/ TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
/ TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
/ FILE REFERENCE: 38-21(53223)B
/ CURRENT APPLICATION NUMBER: US/10/424,599
/ CURRENT FILING DATE: 2003-04-28
/ NUMBER OF SEQ ID NOS: 285684
/ SEQ ID NO 100851
/ LENGTH: 260
/ TYPE: DNA
/ ORGANISM: Glycine max
/ FEATURE:
/ OTHER INFORMATION: Clone ID: PAT_MRT3847_62081C.1
US-10-424-599-100851
```

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Query Match          4.6%; Score 46.4; DB 17; Length 260;
Best Local Similarity 52.6%; Pred. No. 6.6;
Matches 101; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 249 AGAATATATGCTTAATCTTCACTGACATATTAAGTGAATAATGATCAATTTCTTA 308
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 1 ATAACTGTATATCTTTTAAACATTTTATGCAAAAAGACATGAAGTTTCGA 60
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 309 AGATATGCAATATGTTTATTAAGAATGAACTGATTTTGAAGTCAATATCCCAAAA 368
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 61 AAAAAGAGAAATATAGTTTCAAGTTCCTTCTACCTGAAATTTTAAACATCAAC 120
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 369 CATTTGAGATGTTCTGAGCTGAATAATTAACCATTTGAGTGTATTTGAGATGAGATTA 428
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 121 CGTTTGATTTTAAAAAATGACATTAACAAAGTTGTATCTTAAGGGGGGAAA 180
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 429 ATTATTAAGACT 440
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 181 AAACCTTACTACT 192
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
```

Search completed: March 1, 2005, 08:28:53
Job time : 696 secs

| Query Match | Similarity | 100.0% | Score | 1008 | DB | 4 | Length | 1008 |
|-------------|------------|---|-----------|------------|----|--------|--------|------|
| Best Local | Similarity | 100.0% | Pred. No. | 6.7e-244 | | | | |
| Matches | 1008 | Conservative | 0 | Mismatches | 0 | Indels | 0 | Gaps |
| Qy | 1 | ATGGTATACAAATTAAACCTTGATGATGAAGATGATATCCACCCTTGAAAGCAATA | 60 | | | | | |
| Db | 1 | ATGGTATACAAATTAAACCTTGATGATGAAGATGATATCCACCCTTGAAAGCAATA | 60 | | | | | |
| Qy | 61 | GCAGGGAATATGTACGTATCTTAACCTTTAAGCAAACAGATGAGGTCATACAGCATCA | 120 | | | | | |
| Db | 61 | GCAGGGAATATGTACGTATCTTAACCTTTAAGCAAACAGATGAGGTCATACAGCATCA | 120 | | | | | |
| Qy | 121 | TATGGAATGAATATCGAGCTAAGAAATAATATATAGCTTACGCTTTGGCTGAAGTGT | 180 | | | | | |
| Db | 121 | TATGGAATGAATATCGAGCTAAGAAATAATATATAGCTTACGCTTTGGCTGAAGTGT | 180 | | | | | |
| Qy | 181 | ATTGATATATGATCTTAAACTTCTCGATGACTTATTAAAGATAAAGAGACTGCTGAGGA | 240 | | | | | |
| Db | 181 | ATTGATATATGATCTTAAACTTCTCGATGACTTATTAAAGATAAAGAGACTGCTGAGGA | 240 | | | | | |
| Qy | 241 | ATTATCAAGATATATATGCTAATGCTTACATCTGCACATTAAGGTAAGAAATGCTGATCAA | 300 | | | | | |
| Db | 241 | ATTATCAAGATATATATGCTAATGCTTACATCTGCACATTAAGGTAAGAAATGCTGATCAA | 300 | | | | | |
| Qy | 301 | ATTTCTAAAGATATGGCAATGCTTTTATTAAGATGAACCTGATTTGAAAGTCAATAT | 360 | | | | | |

Db 301 ATTCTAAAGATATGCGAAATGCTTTTATATAGATGAACGTGATTTTGAAGCTCAATAT 360
Qy 361 CCTCAAAACATTTGGATATGTTCTTGAGCTGAAATATAACCATATGATGCTTATTCAGAT 420
Db 361 CCTCAAAACATTTGGATATGTTCTTGAGCTGAAATATAACCATATGATGCTTATTCAGAT 420
Qy 421 GACGATTAATTTATGACATATATTTTCTCTGTCAGGAAATTCGACGAGGAAAT 480
Db 421 GACGATTAATTTATGACATATATTTTCTCTGTCAGGAAATTCGACGAGGAAAT 480
Qy 481 CAACATCAAAATGCGCAAGATTTTAAATTAATGATTTCTATTTTACCTTATCTGCT 540
Db 481 CAACATCAAAATGCGCAAGATTTTAAATTAATGATTTCTATTTACCTTATCTGCT 540
Qy 541 GTAATCTCACTGGAGAGAGATTTTTCGAAATACTTTTACATGATGATGAGCTAAA 600
Db 541 GTAATCTCACTGGAGAGAGATTTTTCGAAATACTTTTACATGATGATGAGCTAAA 600
Qy 601 TCATTAGAGATTTATATGAGAGAAAAAACTTTCTPAACTTTCTTTCGACCGCAG 660
Db 601 TCATTAGAGATTTATATGAGAGAAAAAACTTTCTPAACTTTCTTTCGACCGCAG 660
Qy 661 AGATTACCTGATGCGAGATATGTTTGGCTGAGCAACAGAGCGCTTAAATGAGAA 720
Db 661 AGATTACCTGATGCGAGATATGTTTGGCTGAGCAACAGAGCGCTTAAATGAGAA 720
Qy 721 GTGAGTTTAAAGACTTAAATAACAATCTAGAGATGATTTCTAATATGAGAGG 780
Db 721 GTGAGTTTAAAGACTTAAATAACAATCTAGAGATGATTTCTAATATGAGAGG 780
Qy 781 GCTGCAAAACAAAATATATGTTTATTAATAAGAGTACAAAAGGTTAACGCTCCACAG 840
Db 781 GCTGCAAAACAAAATATATGTTTATTAATAAGAGTACAAAAGGTTAACGCTCCACAG 840
Qy 841 ACAGCAGGAGAAAGTTTGGTACAGCAGTGGAGATACCTGAGAAATTCGCGATAT 900
Db 841 ACAGCAGGAGAAAGTTTGGTACAGCAGTGGAGATACCTGAGAAATTCGCGATAT 900
Qy 901 TTATATAGTGTGAGGCTAAGCCAAAAGACAGGGTAACTTTTCTCAAAATGATCTGAC 960
Db 901 TTATATAGTGTGAGGCTAAGCCAAAAGACAGGGTAACTTTTCTCAAAATGATCTGAC 960
Qy 961 AATACATGACGGTTCATATGTTGGAACCTATTATPAAATATATGA 1008
Db 961 AATACATGACGGTTCATATGTTGGAACCTATTATPAAATATATGA 1008

RESULT 2
US-09-463-048A-1
Sequence 1, Application US/09463048A
Patent No. 6630619
GENERAL INFORMATION:
APPLICANT: Commonwealth Scientific and Industrial Research Organisation
APPLICANT: EAST, Peter David
TITLE OF INVENTION: Toxin Genes from the Bacteria *Xenorhabdus nematophilus* and *Photobacterium*
FILE REFERENCE: 050179-0076
CURRENT APPLICATION NUMBER: US/09/463,048A
PRIOR FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: PCT/AU98/00562
PRIOR FILING DATE: 1998-07-17
PRIOR APPLICATION NUMBER: PO 8088
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 1107
TYPE: DNA
ORGANISM: *Xenorhabdus nematophilus*
US-09-463-048A-1

Query Match 65.9%; Score 663.8; DB 4; Length 1107;
Best Local Similarity 79.4%; Pired. No. 2.6e-157;

Matches 835; Conservative 0; Mismatches 162; Indels 54; Gaps 2;
Qy 12 ATTACACCTGATGATAGATGATATATCCACCGCTTGAAGCAATATGACGAGATAT 71
Db 57 AGTAAAGCTGATGATAGATGATATATCCACCGCTTGAAGCAATATGACGAGATAT 116
Qy 72 AGTAAAGCTGATGATAGATGATATATCCACCGCTTGAAGCAATATGACGAGATAT 131
Db 117 AATAGGATGATGATAGATGATATATCCACCGCTTGAAGCAATATGACGAGATAT 176
Qy 132 AATAGGATGATAGATGATATATCCACCGCTTGAAGCAATATGACGAGATAT 191
Db 177 AATAGGATGATAGATGATATATCCACCGCTTGAAGCAATATGACGAGATAT 236
Qy 192 ATCTAAATCTCTGATGATATATGATGATGATGATGATGATGATGATGATGAT 251
Db 237 CTCTCAATCTCTGATGATATATGATGATGATGATGATGATGATGATGATGAT 296
Qy 252 ATATATGCTATATCTTCACTGATGATGATGATGATGATGATGATGATGAT 311
Db 297 ATATATGCTATATCTTCACTGATGATGATGATGATGATGATGATGATGAT 356
Qy 312 TATGCAATATGATTTTATAGATGATGATGATGATGATGATGATGATGAT 371
Db 357 TATGCAATATGATTTTATAGATGATGATGATGATGATGATGATGATGAT 416
Qy 372 TTGATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 431
Db 417 CTGATGATGCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 476
Qy 432 ATTAGCAATATATTTTCTCTGATGATGATGATGATGATGATGATGATGAT 491
Db 477 ATTAGCAATATATTTTCTCTGATGATGATGATGATGATGATGATGATGAT 536
Qy 492 TCCCGCAATTTTATATATGATGATGATGATGATGATGATGATGATGAT 551
Db 537 TCCCGCAATTTTATATATGATGATGATGATGATGATGATGATGATGAT 596
Qy 552 GGGAGAGAGATTTTTCGAAATATTTTACATGATGATGATGATGATGATGAT 611
Db 597 GGGAGAGAGATTTTTCGAAATATTTTACATGATGATGATGATGATGATGAT 656
Qy 612 TTATATGAGAGAGAGATTTTCTPAACTTTCTTTCGACCGCAGATATCTGTA 671
Db 657 TTATATGAGAGAGAGATTTTCTPAACTTTCTTTCGACCGCAGATATCTGTA 716
Qy 672 TGGCAGATATGATTTTGGCTGACCAAGAGAGAGAGAGAGAGAGAGAGAG 714
Db 717 TGGCAGATATGATTTTGGCTGACCAAGAGAGAGAGAGAGAGAGAGAGAG 776
Qy 715 -----TGAG 740
Db 777 TACAGCAACAGCTTACAGAGCTTCAATATGAGAGAGAGAGAGAGAGAGAG 836
Qy 741 AATATCAAAATCTAGAGATGATTTTCTAATATGAGAGAGAGAGAGAGAGAG 800
Db 837 AGATATCAAAATCTAGAGATGATTTTCTAATATGAGAGAGAGAGAGAGAGAG 896
Qy 801 TTATATTTAAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 860
Db 897 TTATATTTAAAGAGATGATGATGATGATGATGATGATGATGATGATGAT 956
Qy 861 TACAGCAGTGGCAGATGATGATGATGATGATGATGATGATGATGATGAT 917
Db 957 TACAGCAGTGGCAGATGATGATGATGATGATGATGATGATGATGATGAT 1016
Qy 918 AAGCAAAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 977
Db 1017 AAGCAAAAGAGAGAGATGATGATGATGATGATGATGATGATGATGATGAT 1076
Qy 978 TAGGTGAGATCTATTAATAATATATGA 1008
Db 1077 AAGGTGAGATCTATTAATAATATATGA 1107

| Query | Match | Best Local Similarity | Matches | Score | DB | Length |
|------------------|---|-----------------------|---------|------------------------------|--------|--------|
| US-09-463-048A-5 | Sequence 5, Application US/09463048A | 65.9% | 79.4% | 663.8 | 671 | 1205 |
| US-09-463-048A-5 | Patent No. 6630619 | 79.4% | 79.4% | 663.8 | 671 | 1205 |
| US-09-463-048A-5 | GENERAL INFORMATION: | 79.4% | 79.4% | 663.8 | 671 | 1205 |
| US-09-463-048A-5 | APPLICANT: Commonwealth Scientific and Industrial Research Organisation | 79.4% | 79.4% | 663.8 | 671 | 1205 |
| US-09-463-048A-5 | APPLICANT: EAST, Peter David | 79.4% | 79.4% | 663.8 | 671 | 1205 |
| US-09-463-048A-5 | TITLE OF INVENTION: Toxin Genes from the Bacteria <i>Xenorhabdus nematophilus</i> and <i>Photobacterium</i> | 79.4% | 79.4% | 663.8 | 671 | 1205 |
| US-09-463-048A-5 | TITLE OF INVENTION: <i>luminiscens</i> | 79.4% | 79.4% | 663.8 | 671 | 1205 |
| US-09-463-048A-5 | FILE REFERENCE: 050179-0076 | 79.4% | 79.4% | 663.8 | 671 | 1205 |
| US-09-463-048A-5 | CURRENT APPLICATION NUMBER: US/09/463, 048A | 79.4% | 79.4% | 663.8 | 671 | 1205 |
| US-09-463-048A-5 | CURRENT FILING DATE: 2002-12-13 | 79.4% | 79.4% | 663.8 | 671 | 1205 |
| US-09-463-048A-5 | PRIOR APPLICATION NUMBER: PCT/AU98/00562 | 79.4% | 79.4% | 663.8 | 671 | 1205 |
| US-09-463-048A-5 | PRIOR FILING DATE: 1998-07-17 | 79.4% | 79.4% | 663.8 | 671 | 1205 |
| US-09-463-048A-5 | PRIOR APPLICATION NUMBER: PO 8088 | 79.4% | 79.4% | 663.8 | 671 | 1205 |
| US-09-463-048A-5 | PRIOR FILING DATE: 1997-07-17 | 79.4% | 79.4% | 663.8 | 671 | 1205 |
| US-09-463-048A-5 | NUMBER OF SEQ ID NOS: 20 | 79.4% | 79.4% | 663.8 | 671 | 1205 |
| US-09-463-048A-5 | SOFTWARE: PatentIn version 3.1 | 79.4% | 79.4% | 663.8 | 671 | 1205 |
| US-09-463-048A-5 | SEQ ID NO 5 | 79.4% | 79.4% | 663.8 | 671 | 1205 |
| US-09-463-048A-5 | LENGTH: 1205 | 79.4% | 79.4% | 663.8 | 671 | 1205 |
| US-09-463-048A-5 | TYPE: DNA | 79.4% | 79.4% | 663.8 | 671 | 1205 |
| US-09-463-048A-5 | ORGANISM: <i>Xenorhabdus nematophilus</i> | 79.4% | 79.4% | 663.8 | 671 | 1205 |
| Query Match | Best Local Similarity | Matches | Score | DB <td>Length</td> <td></td> | Length | |
| 65.9% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 79.4% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 0 | 0 | 162 | 54 | 54 | 54 | |
| 65.9% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 79.4% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 0 | 0 | 162 | 54 | 54 | 54 | |
| 65.9% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 79.4% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 0 | 0 | 162 | 54 | 54 | 54 | |
| 65.9% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 79.4% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 0 | 0 | 162 | 54 | 54 | 54 | |
| 65.9% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 79.4% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 0 | 0 | 162 | 54 | 54 | 54 | |
| 65.9% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 79.4% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 0 | 0 | 162 | 54 | 54 | 54 | |
| 65.9% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 79.4% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 0 | 0 | 162 | 54 | 54 | 54 | |
| 65.9% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 79.4% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 0 | 0 | 162 | 54 | 54 | 54 | |
| 65.9% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 79.4% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 0 | 0 | 162 | 54 | 54 | 54 | |
| 65.9% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 79.4% | 79.4% | 0 | 663.8 | 671 | 1205 | |
| 0 | 0 | 162 | 54 | 54 | 54 | |
| 65.9% | 79.4% | 0 | 663.8 | 671 | | |

| | | | | |
|--|-----------------|---|------------------------------------|--------------|
| Qy | 672 | TGGCAGAAATAGTATTATTTGGCTGACCAACGAGCGCTTAA | ----- | 714 |
| Db | 733 | TGGCAGAAACAGGCTACTTGGCCGGTCCAAACAAAGCGCTTAA | TTTCCAAACAGCCTTTC | 792 |
| Qy | 715 | ----- | TGGAGCTGAGTTTAAAGAACTTAA | 740 |
| Db | 793 | TACAGCAACACGCTCTACAGAGCTTCATCTAA | TTTGGAGAGATTGTTTGCACAAACCTTAG | 852 |
| Qy | 741 | AAATPACAAATCTAGGAATGATTTTCTA | AATGGAAGGGCTCGAATAACAAAGTATAG | 800 |
| Db | 853 | AGATPACCCATCCAGAAATATACATTATG | AAATGAAATGATGATCTCGCAAAACGAAATATAG | 912 |
| Qy | 801 | TTCAATTTATAAAGGATPACAAAAGGGTAA | CGCTCCACAGACAGCGAAGAAATATTGG | 860 |
| Db | 913 | TTCAATTTATAAAGGATPACAAAAGGGTAA | TGATTCACGTGACAGCAGCAGATTTGG | 972 |
| Qy | 861 | TACAGCCAGTGGCAGTAACTCTGAAAAAT | TTGCCGAMTA--ATTATATAGTGTGAGGCT | 917 |
| Db | 973 | TACAAAAAGCGGACGTAACCTTGCAAAA | CTGCAGAGTGAATTTATATAGATTAAGCT | 1033 |
| Qy | 918 | AAGCCAAAAGACACGGGTAACCTTACTCA | AAATGATCTGCAATACAAATGACGGTTCA | 977 |
| Db | 1033 | AAGCCAAAGAACACGGGTAACCTTCCAT | AAATATATCTGACCAAAATATGAGATCA | 1092 |
| Qy | 978 | TAGTGTGGAACCTCATTTATAAAATATAT | TATGTA 1008 | |
| Db | 1093 | AAGTGTGGAACCTCATTTCCAAAATATAT | TAA 1123 | |
| <p>RESULT 4 US-08-569-168-6 Sequence 6, Application US/08569168 Patent No. 5872687 GENERAL INFORMATION: APPLICANT: Smigielski, Adam J. APPLICANT: Akhurst, Raymond J. TITLE OF INVENTION: TOXIN GENE FROM XENORHABDUS NEMATOPHILUS NUMBER OF SEQUENCES: 7 CORRESPONDENCE ADDRESS: ADDRESSES: Lowe, Price, Leblanc & Becker STREET: 99 Canal Center Plaza, Suite 300 CITY: Alexandria STATE: VA COUNTRY: USA ZIP: 22314 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patent In Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/569,168 FILING DATE: CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: NAME: Price, Robert L. REGISTRATION NUMBER: 22,685 REFERENCE/DOCKET NUMBER: 1451-015 TELECOMMUNICATION INFORMATION: TELEPHONE: 703-684-1111 INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 1272 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) US-08-569-168-6</p> | | | | |
| Query Match | 62.3% | Score 628.2; | DB 2; | Length 1272; |
| Best Local Similarity | 79.1% | Pred. No. 2.5e-148; | | |
| Matches 833; | Conservative 0; | Mismatches 163; | Indels 57; | Gaps 5; |

QY 12 ATTAACACCTGATGATGAGATGATCCACCGTTGAAAACAAATAGCAGAGATAT 71
| | | | |
Db 139 AGTAACGCGCTGATGATGAGATGATCAACCGTTGAAAACAAATAGCAGAGATAT 198
| | | | |
QY 72 AGTACGTAATCTAACTTTAGCAACAGATGAGGCTCATACGATCATATGGAATTGA 131
| | | | |
Db 199 AATACGTAATCTAACTTTAGCAACAGATGAGGCTCATACGATCATATGGAATTGA 258
| | | | |
QY 132 ATATGAGCTAAGAAATATATTTAGCTTACGCTTTGGCTGTAAGGTTATCATATGT 191
| | | | |
Db 259 ATATGAGCTAAGAAATATATTTAGCTTACGCTTTGGCTGTAAGGTTATCATATGT 318
| | | | |
QY 192 ATCTAACTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 251
| | | | |
Db 319 CTCTCAACTCTCGAAGACATATTTAATAATAGATGATGATGATGATGATGATGAT 378
| | | | |
QY 252 ATATATGCTAATCTTTATCTGATGATGATGATGATGATGATGATGATGATGAT 311
| | | | |
Db 379 ATATATGCTAATCTTTATCTGATGATGATGATGATGATGATGATGATGATGAT 438
| | | | |
QY 312 TATGCAATGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 371
| | | | |
Db 439 TATGCAATGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 497
| | | | |
QY 372 TTGGAATGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 430
| | | | |
Db 498 CTGGAATATCTCGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 557
| | | | |
QY 431 TATTAACATATATTTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 490
| | | | |
Db 558 TATTAACATATATTTTCTGATGATGATGATGATGATGATGATGATGATGATGAT 617
| | | | |
QY 491 ATGCGCAAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 550
| | | | |
Db 618 ATGCGCAAGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 677
| | | | |
QY 551 TGGGAAGAGATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 610
| | | | |
Db 678 TGGGAAGAGATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 737
| | | | |
QY 611 ATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 670
| | | | |
Db 738 ATTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 797
| | | | |
QY 671 ATGCGCAAGATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 714
| | | | |
Db 798 ATGCGCAAGATTTTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 857
| | | | |
QY 715 -----TGAAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 738
| | | | |
Db 858 CTACAGCAACAGCTCTACAGCAAGCTCTACATGATGATGATGATGATGATGATGAT 917
| | | | |
QY 739 AAAATATACAAATCTAGAAATGATGATGATGATGATGATGATGATGATGATGAT 798
| | | | |
Db 918 AGAGATACCAATCTAGAAATGATGATGATGATGATGATGATGATGATGATGAT 977
| | | | |
QY 799 AGTCAATTTATTAAGAGTACAAAGGATGATGATGATGATGATGATGATGATGATGAT 858
| | | | |
Db 978 AGTCAATTTATTAAGAGTACAAAGGATGATGATGATGATGATGATGATGATGATGAT 1037
| | | | |
QY 859 GGTACAGCAGTGGAGTACCTGAAAATTTGCCGATA---ATTATATAGTGTGAG 915
| | | | |
Db 1038 GGTACAGCAGCAGTGGAGTACCTGAAAATTTGCCGATA---ATTATATAGTGTGAG 1097
| | | | |
QY 916 CTAAAGCAAAAGACAGGGTAACTTAAATGATGATGATGATGATGATGATGATGATGAT 975
| | | | |
Db 1098 CTAAAGCAAAAGACAGGGTAACTTAAATGATGATGATGATGATGATGATGATGATGAT 1157
| | | | |
QY 976 CATAGTGTGAGTCTATTTATTAATGATGATGATGATGATGATGATGATGATGATGAT 1008
| | | | |
Db 1158 CAAAGTGTGAGTCTATTTATTAATGATGATGATGATGATGATGATGATGATGATGAT 1190
| | | | |

RESULT 5
US-08-569-168-3
; Sequence 3, Application US/08569168
; Patent No. 5972687
; GENERAL INFORMATION:
; APPLICANT: Smlglski, Adam J.
; APPLICANT: Ahlberg, Raymond J.
; TITLE OF INVENTION: TOXIN GENE FROM XENORHABDUS NEMATOPHILUS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lowe, Price, Leblanc & Becker
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: VA
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,168
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Price, Robert L.
; REGISTRATION NUMBER: 22,685
; REFERENCE/DOCKET NUMBER: 1451-015
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-684-1111
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 834 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-569-168-3
Query Match 51.7%; Score 521.4; DB 2; Length 834;
Best Local Similarity 85.4%; Pred. No. 1.5e-121;
Matches 604; Conservative 0; Mismatches 101; Indels 2; Gaps 2;
QY 12 ATTAACACCTGATGATGAGATGATCCACCGTTGAAAACAAATAGCAGAGATAT 71
| | | | |
Db 57 AGTAACGCGCTGATGATGAGATGATCAACCGTTGAAAACAAATAGCAGAGATAT 116
| | | | |
QY 72 AGTACGTAATCTAACTTTAGCAACAGATGAGGCTCATACGATCATATGGAATTGA 131
| | | | |
Db 117 AATACGTAATCTAACTTTAGCAACAGATGAGGCTCATACGATCATATGGAATTGA 176
| | | | |
QY 132 ATATGAGCTAAGAAATATATTTAGCTTACGCTTTGGCTGTAAGGTTATCATATGT 191
| | | | |
Db 177 ATATGAGCTAAGAAATATATTTAGCTTACGCTTTGGCTGTAAGGTTATCATATGT 236
| | | | |
QY 192 ATCTAACTCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 251
| | | | |
Db 237 CTCTCAACTCTCGAAGACATATTTAATAATGATGATGATGATGATGATGATGATGAT 296
| | | | |
QY 252 ATATATGCTAATCTTTATCTGATGATGATGATGATGATGATGATGATGATGATGAT 311
| | | | |
Db 297 ATATATGCTAATCTTTATCTGATGATGATGATGATGATGATGATGATGATGATGAT 356
| | | | |
QY 312 TATGCAATGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 371
| | | | |
Db 357 TATGCAATGCTTTTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 415
| | | | |
QY 372 TTGGAATGCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 430
| | | | |
Db 416 CTGGAATATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 475
| | | | |

| | Query Match | Similarity | Score | DB 2 | Length |
|------------|-------------|---|-------|----------------|----------|
| Best Local | 85.4% | Pred. NO. 1.6e-121 | | | |
| Matches | 604 | Conservative | 0 | Mismatches 101 | Indels 2 |
| | | | | | Gaps 2 |
| Qy | 12 | ATTACACCTCATGTAGTAGTGATATCCACCCCTGTAAAAAGCAATATGACAGAGAT | 71 | | |
| Db | 57 | AGTACGCCCTATGATTAAGATGATATATCCACCCGTGTAAAAAGCAATATGACGGAGAT | 116 | | |
| Qy | 72 | AGTACGATATCTAACTTTAAGCAACAGATGAGGCTCATACGATCATATGTGAATTGA | 131 | | |
| Db | 117 | AATACGTCTACTAGAAATTCACAGCAAAATGAAGAATCATACGAGATTTGTTGGAATTC | 176 | | |

```
Query Match      6.2%; Score 62.6; DB 4; Length 1141;
Best Local Similarity 11.1%; Pred. No. 4.4e-06;
Matches      81; Conservative 280; Mismatches 360; Indels 6; Gaps 1;
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Oy 185 ATATGATCTAAACTTCGTGACTATTATAGATATAAGAGACTGCTGAGAGATT 244
 |:-|-:::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|:
db 834 ACACCTTAAABWBGWSGCCNNNNNNNNNNNNNNNCHYTTANABB CYRANNNNNAAMARIC 775

```

Qy 245 ATCAAGATATATGTCTAACTTTCATCTGCACTATTAAGTGAATAATGTCATTAATTT 304
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 774 NNYYMAAAVTTTTHDWCYKTMNTWYDMWTMTTTRMTTSTNNNNNNNNMACCTNN 715
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 305 CTAAGAATATGCAAAATGTTTATAGAATGATGATTTTGAAGTCAATATCTTC 364
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 714 NNNNNMKAAYAAATNNMGMNNTDARRTNTTVMRRMTNTKTWSTTRRHHTGAT 655
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 365 AAAACATTTGAAATGTTCTGAGCTGAAAATAAACATTTAGTGTATTT-----CAG 418
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 654 NNNNNNNNNNNNNNNNNNSCTCTRMATMTMTKDGMTTKKVMRTTCTTVDVWADSV 595
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 419 ATGACGATTAATTTATGACATATTTTCTCTGTAAGAAATTTCACTGAGAGAA 478
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 594 WMYANMRCRDVLTNTNTYCKSYASVYMSNNAMWYRYSABNNSMAWRTTRNNMM 535
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 479 ATCAACAATCAATGCGCAAGATTTTAAATTAATGATTTCTTATTTACTTATCTG 538
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 534 SGBVRMRWAGTMMWRMNNNTDTRYYMWRKWARBTITYDSMCNAKSMWRGNMRRAMK 475
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 539 CTGTACTTCACTGAGAGAGATTTTCAAAAACTTTTCAATGATTAAGAGCTA 598
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 474 MMYAANNDAGADHTWYMGNTMWRRAKMMNMACRRATCCNNNNNACVHHKXMM 415
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 599 AATCATTAAGAAATTAATTTAGAGAAAAAATTTCTAACTTTCTTTCAGCACCCG 658
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 414 RMTWKMWKAACNNNNBKAMMYRVAMMYSDTTNTDMMWTSDDMHMYTVDYTMWRAM 355
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 659 AGAGATTAAGTATGCGAATATGTTATTTGGCTGACCAAGAGAGGCTTAATTTGA 718
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 354 NNNNNNNMBCKTSMWMMWDHNTCTYGNNTGSAYBMAAASMAAGASBVTYNNMCM 295
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 719 GAGTGAATTTAAAGAACTTAATAAATCTAAGATGATTTTCTTAATTAAGGA 778
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 294 RMTWKTMTNNNNNNKAMTYRTKYTAMCNRTYTDPAVTEGNTKYCTAIBWYBMM 235
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 779 GGGCTGCAAAACAAAATAGTTACTTTATTAAGAGATACAAAAGGTAACGCTCCAC 838
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 234 GKHHMWRBRABHRSNNMMWVKCRNKYMSWYHARBYBMAVOCNNNMVORAHNNH 175
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 839 AGACAGCAGGAAAAGATTTGTAAGCCAGTGCAGTGAAGTGAAGGATTTCCGAAAT 898
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 174 CATNNNNMMWYAYMHMHKKGAAATNKTARDBAHVKTWYMYRYDYCAMCMMA 115
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 899 ATTATA 905
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 114 KAKVTA 108
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

```

; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,313
; FILING DATE:
; APPLICATION NUMBER: EP 91 114 300.6
; FILING DATE: 26-AUG-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 30472/114 IMMU
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7218 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; CLONE: pTZapC-F18
;
US-08-232-463-14
Query Match 5.9%; Score 59.8; DB 1; Length 7218;
Best Local Similarity 6.0%; Pred. No. 4,3e-05;
Matches 25; Conservative 225; Mismatches 167; Indels 0; Gaps 0;

Qy 521 TCTTATTAACCTTATCTGCTGTAACCTGCACTGGAAGAGATTTTCAAAAACTTTT 580
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1484 TGTAAATTAACCTATCTATGCAAGTAGTTAAAGATAGAAATTTGTACRRRRRRRR 1425
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 581 ACAATGATTAAGAGCTAAATCATTAAGAATTAATTTAGAGAAAAAACTTTTAAC 640
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1424 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1365
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 641 CTTTCTTTGACCAAGAGATTAACCTGATGAGATAGATTGCTGAGACCA 700
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1364 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1305
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 701 CAGAAAGCGCTTAATGAGAGAGTGAATTTAAAGAACTTAATAAACAATCTAGAAATG 760
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1304 RRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRRR 1245
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 761 GATTTTCAATATGAGAGGGCTGCAAAAACAAAGTATAGTTTATTAAGAGTAC 820
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
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RESULT 9
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; Sequence 23, Application US/09806708B
; Patent No. 6784342
; GENERAL INFORMATION:
; APPLICANT: The University of British Columbia
; TITLE OF INVENTION: Regulation of Embryonic Transcription in Plants
; FILE REFERENCE: 4810-58741
; CURRENT APPLICATION NUMBER: US/09/806,708B
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: US 60/147,133
; PRIOR FILING DATE: 1999-08-04
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 23

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 1, 2005, 02:23:47 ; Search time 4591 Seconds
(without alignments)
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Listing first 45 summaries

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RESULT 2

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US-10-617-962-1
; Sequence 1, Application US/10617962
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Research Organisation
; APPLICANT: EAST, Peter David
; TITLE OF INVENTION: Toxin Genes from the Bacteria Xenorhabdus nematophilus and Photoc
; FILE REFERENCE: 050179-0076
; CURRENT APPLICATION NUMBER: US/10/617,962
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US/09/463,048A
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PCT/AU98/00562
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: PO 8088
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 1107
; TYPE: DNA
; ORGANISM: Xenorhabdus nematophilus
US-10-617-962-1

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Query Match 65.9%; Score 663.8; DB 58; Length 1107;
Best Local Similarity 79.4%; Pred. No. 1.4e-135;
Matches 835; Conservative 0; Mismatches 162; Indels 54; Gaps 2;

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; Sequence 5, Application US/10617962
; GENERAL INFORMATION:
; APPLICANT: Commonwealth Scientific and Industrial Research Organisation
; APPLICANT: EAST, Peter David
; TITLE OF INVENTION: Toxin Genes from the Bacteria Xenorhabdus nematophilus and Photoc
; FILE REFERENCE: 050179-0076
; CURRENT APPLICATION NUMBER: US/10/617,962
; CURRENT FILING DATE: 2003-07-14
; PRIOR APPLICATION NUMBER: US/09/463,048A
; PRIOR FILING DATE: 2002-12-13
; PRIOR APPLICATION NUMBER: PCT/AU98/00562
; PRIOR FILING DATE: 1998-07-17
; PRIOR APPLICATION NUMBER: PO 8088
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn version 3.1

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Db 1124 RRR 1068

RESULT 5
PCT-US99-26796-234
; Sequence 234, Application PC/TUS9926796
; GENERAL INFORMATION:
; APPLICANT: United States Government as Represented by the
; APPLICANT: Secretary of the Navy
; TITLE OF INVENTION: Chromosome 2 Sequence of Human Malaria Parasite
; TITLE OF INVENTION: Plasmodium falciparum and Proteins of Said
; TITLE OF INVENTION: Chromosome Useful in Anti-malarial Vaccines and
; TITLE OF INVENTION: Diagnostic Reagents
; FILE REFERENCE:
; CURRENT APPLICATION NUMBER: PCT/US99/26796
; CURRENT FILING DATE: 1999-11-05
; NUMBER OF SEQ ID NOS: 420
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 234
; LENGTH: 3927
; TYPE: DNA
; ORGANISM: Plasmodium falciparum
PCT-US99-26796-234

Query Match 5.2%; Score 52.6; DB 1; Length 3927;
Best Local Similarity 43.9%; Pred. No. 0.87;
Matches 212; Conservative 0; Mismatches 344; Indels 3; Gaps 1;

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US-10-990-328-94720/C
; Sequence 94720, Application US/10990328
; GENERAL INFORMATION:
; APPLICANT: CARIGIL, Michele
; TITLE OF INVENTION: POLYMORPHISMS IN NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING HUMAN ENZYME PROTEINS, METHODS OF DETECTION AND
; TITLE OF INVENTION: USBS THEREOF
; FILE REFERENCE: CL001495
; CURRENT APPLICATION NUMBER: US/10/990,328
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 558824
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 94720
; LENGTH: 709368
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(709368)
; OTHER INFORMATION: n = A,T,C or G
US-10-990-328-94720

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Best Local Similarity 45.7%; Pred. No. 4.9; Indels 0; Gaps 0;
Matches 169; Conservative 3; Mismatches 198; Indels 0; Gaps 0;

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Db 674525 TAAATTAATTAATTTCAATTTTAATGATTAAGAAATCACTCAATGATCTT 674466
QY 569 CAAAAAATTTTCAATGATTAAGAGCTTAATCAATTAAGATTAATTTAGAGAAA 628
Db 674465 TGCAGTATTTTATCTGTTTATTTACTTAAAGTTACAGAAAGTAACTATATCA 674406
QY 629 AACTTCTAAACCTTTCTTTCGACCCAGAGATTTACTGAGCAAAATAGTTAT 688
Db 674405 TCTTTATTTGCTGCTCTTTTAAATTTTGTATTTCTCCCTCCAGATTTAG 674346
QY 689 TGGCTGACCAAGAAAGGCTTAATGAGAGTGAATTTAAAGACTTAATAATPA 748
Db 674345 GATGAAATCGAGAAATTAAGCTGAATTTATCTATKTCVTTATATTAATAA 674286
QY 749 AATCTGAATGATTTCTTAATATGAAAGGGCTGCAAAACAAAGTATATGTTCA 808
Db 674285 ATTTTAAGTATGATTTTAAAGATTTGTTGACATATACCTCCAGTGTGACCT 674226
QY 809 TAAAGAGGT 818
Db 674225 ATTAAGAGGT 674216


```
; GENERAL INFORMATION:
; APPLICANT: OLEK, Alexander
; APPLICANT: PIEPENBROCK, Christian
; APPLICANT: BERLIN, Kurt
; TITLE OF INVENTION: Diagnosis of Diseases Associated with DNA
; TITLE OF INVENTION: Transcription
; TITLE OF INVENTION: by Means of Assessing the Methylation Status of Genes Associated
; FILE REFERENCE: 5013.1009
; CURRENT APPLICATION NUMBER: US/10/240,453
; CURRENT FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: PCT/EP01/03973
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: DE 10019058.8
; PRIOR FILING DATE: 2000-04-06
; PRIOR APPLICATION NUMBER: DE 10019173.8
; PRIOR FILING DATE: 2000-04-07
; PRIOR APPLICATION NUMBER: DE 10032529.7
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: DE 10043826.1
; PRIOR FILING DATE: 2000-09-01
; NUMBER OF SEQ ID NOS: 350
; SEQ ID NO 95
; LENGTH: 11394
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-240-453-95
```

```
Query Match      4.9%; Score 49.8; DB 50; Length 11394;
Best Local Similarity 50.6%; Pred. No. 4.8;
Matches 120; Conservative 0; Mismatches 117; Indels 0; Gaps 0;

QY 124 GGAATGATATGACCTAAGAAATATATAGCTTACCTTGGCTGATGATTT 183
    |||||
DB 318 GGAATGATATGAGGTGTAAGATATATAGAAATATATAGTTAGTTATAGATATATAT 377

QY 184 CATATGATATCTAACTTCCCTGATGACATTTATATAGAAATTAAGACATGCTGAGAAATTT 243
    |||||
DB 378 ATATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 437

QY 244 TATCAAGATATATATGCTTAATCTTTCATCTGACATATAGGTAAGAAATGCTGATCAAAATTT 303
    |||||
DB 438 AAGGTTAGATATATATATATATATATATATATATATATATATATATATATATATATAT 497

QY 304 TCTAAGATATGCAATATGTTTATATAGAAATGAACTGATTTTGAAGTCAATAT 360
    |||||
DB 498 TGATATTTTATATAGTATATATATATATATATATATATATATATATATATATATATAT 554
```

RESULT 12
US-09-948-124-61

```
; Sequence 61, Application US/09948124
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON CH
; TITLE OF INVENTION: Y. METHODS OF DETECTION, AND USES THEREOF
; FILE REFERENCE: CL001301
; CURRENT APPLICATION NUMBER: US/09/948,124
; CURRENT FILING DATE: 2002-12-23
; NUMBER OF SEQ ID NOS: 183
; SEQ ID NO 61
; LENGTH: 318007
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)... (318007)
; OTHER INFORMATION: n = A,T,C or G
US-09-948-124-61
```

Query Match 4.9%; Score 49.8; DB 41; Length 318007;

```
Best Local Similarity 46.6%; Pred. No. 12;
Matches 159; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

QY 108 TCATCAGCATCATATGCAATATGATATGCAATGAAATTAATATAGCTTACGCTTT 167
    |||||
DB 133261 TATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 133320

QY 168 GCGTGAAGTGTATATCAATATATATATATATATATATATATATATATATATATATATAT 227
    |||||
DB 133321 AATTAATATATATATATATATATATATATATATATATATATATATATATATATATAT 133380

QY 228 GACTGCTGAGAAATTTATCAAGATATATGCTATCTTATCTGCACTATTTAGGCGA 287
    |||||
DB 133381 TATTTAATATATATATATATATATATATATATATATATATATATATATATATATAT 133440

QY 288 AATGCTGATCAAAATTTCTAAAGATATGCAAAATGTTTTTATTAAGAAATGAGATTT 347
    |||||
DB 133441 TATTTATATATATATATATATATATATATATATATATATATATATATATATATATAT 133500

QY 348 TGAAGTCAATATCTCTCAAAATTTGGAATGCTTGAAGCTTGAATTAACCATTTGAG 407
    |||||
DB 133501 TATTAAGTAAATATCTATATATATATATATATATATATATATATATATATATATATAT 133560

QY 408 TGCTTATTCAGATGACATTAATTTATAGCACTATATTTT 448
    |||||
DB 133561 TGTATATATATATATATATATATATATATATATATATATATATATATATATATATAT 133601
```

RESULT 13
US-09-947-911-2

```
; Sequence 2, Application US/09947911
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig
; TITLE OF INVENTION: COLLECTION OF SINGLE NUCLEOTIDE POLYMORPHISM (SNPs) LOCATED ON CH
; TITLE OF INVENTION: X. METHODS OF DETECTION, AND USES THEREOF
; FILE REFERENCE: CL001300
; CURRENT APPLICATION NUMBER: US/09/947,911
; CURRENT FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 368
; SEQ ID NO 2
; LENGTH: 600322
; TYPE: DNA
; ORGANISM: HUMAN
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)... (600322)
; OTHER INFORMATION: n = A,T,C or G
US-09-947-911-2
```

Query Match 4.9%; Score 49.8; DB 41; Length 600322;
Best Local Similarity 46.6%; Pred. No. 14;
Matches 159; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

```
QY 108 TCATCAGCATCATATGCAATATGATATGCAATGAAATTAATATAGCTTACGCTTT 167
    |||||
DB 499869 TATATATATATATATATATATATATATATATATATATATATATATATATATATATAT 499928

QY 168 GCGTGAAGTGTATATCAATATATATATATATATATATATATATATATATATATATATAT 227
    |||||
DB 499929 AATTAATATATATATATATATATATATATATATATATATATATATATATATATATAT 499988

QY 228 GACTGCTGAGAAATTTATCAAGATATATGCTATCTTTCATCTGCACTATTTAGGCGA 287
    |||||
DB 499989 TATTTAATATATATATATATATATATATATATATATATATATATATATATATATATAT 500048

QY 288 AATGCTGATCAAAATTTCTAAAGATATGCAAAATGTTTTTATTAAGAAATGAGATTT 347
    |||||
DB 500049 TATTTATATATATATATATATATATATATATATATATATATATATATATATATATAT 500108

QY 348 TGAAGTCAATATCTCTCAAAATTTGGAATGCTTGAAGCTTGAATTAACCATTTGAG 407
    |||||
DB 500109 TATTAAGTAAATATCTATATATATATATATATATATATATATATATATATATATATAT 500168
```


QY 199 CTTCGATGACTATTAAGATTAAGAGACTGCTGAGAGATTTATCAAGATATATG 258
DB 1934 TAT 1993
QY 259 TCTAATCTTCATCTGCACTATTAGTGAAATGGATCAAAATTTCTAAAGATATGCA 318
DB 1994 TAAAT 2053
QY 319 AATGCTTTTATTAAGATGACGATTTTGAAGGTCATATCCCAAAATTTGGAT 378
DB 2054 TAT 2113
QY 379 GTTCGAGCTTGAATAATCAATGAGTCTTATTCAGATGAGATTAATATATAGCA 438
DB 2114 TATGAT 2173
QY 439 CTATATTTTCTCTGTACAGAAATTCGACGTGAGAAATCAATCAATGCGCA 498
DB 2174 TAT 2233
QY 499 AGATTTTATTAATTAAT 515
DB 2234 TTAATCATTTATATATCAT 2250

RESULT 5

US-10-517-441-307
; Sequence 307, Application US/10517441
; GENERAL INFORMATION:
; APPLICANT: FOKKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMERICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: HOEFER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 307
; LENGTH: 8093
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-307

Query Match 4.0%; Score 40.6; DB 7; Length 8093;
Best local Similarity 43.7%; Pred. No. 2.7; Indels 0; Gaps 0;

Matches 178; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

QY 212 ATTATAGAGATTAAGAGACTGCTGAGAGATTTATCAAGATATATCTTAATCTTTCAAT 271
DB 1467 ATTGATTAATATTTAGAGAGATTTATGAATATTAATTTGGGTTTGGTTTAAATTTAGTTT 1526
QY 272 CTCGACTATTAAGTGAAGATGATCAATTTCTAAAGTATAGCAAAATGGTTTATTA 331

DB 1527 ATATATGAATTTTAAAGATGTTTTTTTATGCGAATAGAGTTTGAATATGTTTT 1586
QY 332 AGAATGAATCTGATTTTGAAGTCAATATCCCAAAACATTTGGAATGTTCCGACTTG 391
DB 1587 GGTATTAAGATTAATTTTATGATGAAATTAATGAAATTTATGTAATTTGGAATGAAATG 1646
QY 392 AAAATTAACCATTTAGTGTCTTATTCAGATGAGATTAATTAATTTAGACTATATTTTCT 451
DB 1647 TTTTAAATATTTTATTTTGTGTGTTATTTATATATAGAAATGATGATGTTTAA 1706
QY 452 CTGTACAGAAATTCACATGAGAGAAATCAATCAATCAATGCGCAATTTTAAAT 511
DB 1707 TTTTGAATTAATTTATTTTATGATTTATTAATTAATTTGATATTTATTTTAAATA 1766
QY 512 TAATGATTTCTTATTTTACCTTATCTGTATCTGTAATCTTCACTGAGAGAGATTTTCA 571
DB 1767 AAGTGTATTTTATTTAGTATGATTTTAAATTAATTAATTAATTTAGTATGATTAAGAT 1826
QY 572 AAACTTTTCAATGATTTAGAGGCTAATATCTATAGAAATTTATAT 618
DB 1827 AAAAAGTTAAATATTTTATATTTTATTTTAAATTTTGAATGTAATTTT 1873

RESULT 6

US-10-517-441-441
; Sequence 441, Application US/10517441
; GENERAL INFORMATION:
; APPLICANT: FOKKENS, John
; APPLICANT: HARBECK, Nadia
; APPLICANT: KOENIG, Thomas
; APPLICANT: MAIER, Sabine
; APPLICANT: MARTENS, John
; APPLICANT: MODEL, Fabian
; APPLICANT: NIMMERICH, Inko
; APPLICANT: RUJAN, Tamas
; APPLICANT: SCHMITT, Armin
; APPLICANT: SCHMITT, Manfred
; APPLICANT: LOOK, Maxime P.
; APPLICANT: HOEFER, Heinz
; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
; FILE REFERENCE: 47675-93
; CURRENT APPLICATION NUMBER: US/10/517,441
; CURRENT FILING DATE: 2004-12-11
; PRIOR APPLICATION NUMBER: PCT/EP2003/010881
; PRIOR FILING DATE: 2003-10-01
; PRIOR APPLICATION NUMBER: DE 10317955.0
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: DE 10300096.8
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: DE 10245779.4
; PRIOR FILING DATE: 2002-10-01
; NUMBER OF SEQ ID NOS: 2147
; SEQ ID NO 441
; LENGTH: 12610
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-441

Query Match 4.0%; Score 40.4; DB 7; Length 12610;
Best local Similarity 45.9%; Pred. No. 3.2; Indels 4; Gaps 1;

Matches 178; Conservative 0; Mismatches 206; Indels 4; Gaps 1;

QY 231 TCTGAGAGATTTATCAAGATTAATGCTTAATCTTCACTGCACTATTAAGTGAATA 290
DB 7753 TGTGAGAGATTAAGATGATTAATGCTTAATTAATTAAGAAATGTTTTTATGAAA 7812
QY 291 TGTATCAAAATTTCTAAAGATATAGCAAAATGTTTTTAAAGATGAATGATTTTGA 350

Db 7813 TATTAAGTAAGTATTATAGTATATGAAATGTTATGGAATTTGTTTGA 7872
Qy 351 AGGTCAATATCCTCAAAAACATTTGGAAATGTTCTGAGCTTGAAATAAACAATTGAGTGC 410
Db 7873 GAGAAATTTTGAATAAATGTTTTTTTATTAATGTTTGAAGTGTGG 7932
Qy 411 TTATTCAGATGACGATTAATTTATTTAGCTATATTTTTCTGTCAGAAATTCCTACT 470
Db 7933 TTTTATAGAAAGTAATAATTAATTAATGATTAAGATTAAGTGTGTTAATGAGCTTTTAA 7992
Qy 471 GGAGGAAATCAACATCAAAATGCCGCAAGATTTTAAATTAATGATTTCTATTTAC 530
Db 7993 ATAGTATTTT---AATTGAAATATGAATATGTTTAAATTAAGATTAATATTTGTT 8048
Qy 531 CTATCTGCTGTAACCTCACTGGAAGAGATTTTTCAAAAAATTTCATGAGAT 590
Db 8049 TAAAAATGTTTTCGTGATGTTTAAATGATTTTGAAGTTTAAATGAAATGTAT 8108
Qy 591 AGAGGCTAAATCATTAAGAAATTAATTT 618
Db 8109 AAATGTATATTAATTAAGATTAATTT 8136

RESULT 7

US-10-517-441-715

; Sequence 715, Application US/10517441

; GENERAL INFORMATION:

; APPLICANT: POEKENS, John

; APPLICANT: HARBEC, Nadia

; APPLICANT: KOENIG, Thomas

; APPLICANT: MAIER, Sabine

; APPLICANT: MARTENS, John

; APPLICANT: MODEL, Fabian

; APPLICANT: NIMMICH, Inko

; APPLICANT: RUJAN, Tamas

; APPLICANT: SCHMITT, Armin

; APPLICANT: SCHMITT, Manfred

; APPLICANT: LOOK, Maxime P.

; APPLICANT: MARX, Almut

; APPLICANT: HOEFER, Heinz

; TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell

; FILE REFERENCE: 47675-93

; CURRENT APPLICATION NUMBER: US/10/517,441

; CURRENT FILING DATE: 2004-12-11

; PRIOR APPLICATION NUMBER: PCT/EP2003/010881

; PRIOR FILING DATE: 2003-10-01

; PRIOR APPLICATION NUMBER: DE 10317955.0

; PRIOR FILING DATE: 2003-04-17

; PRIOR APPLICATION NUMBER: DE 10300096.8

; PRIOR FILING DATE: 2003-01-07

; PRIOR APPLICATION NUMBER: DE 10245779.4

; PRIOR FILING DATE: 2002-10-01

; NUMBER OF SEQ ID NOS: 2147

; SEQ ID NO 715

; LENGTH: 12610

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)

; US-10-517-441-715

Query Match 4.0%; Score 40.4; DB 7; Length 12610;
Best Local Similarity 45.9%; Pred. No. 3.2; Mismatches 206; Indels 4; Gaps 1;
Matches 178; Conservative 0;

Qy 231 TGGCTGAGAAATTTATCAAGATATATGCTTAATCTTCACTGCACTATAGTAAAA 290
Db 7753 TGTGTGAGATTAATGATGATATATATGTTAATTAAGAAATGTTTATTAAGAA 7812
Qy 291 TGGTATCAAAATTTCTAAAGATATGCAAAATGCTTTTATTAAGAAATGCAATGATTTGA 350
Db 7813 TATTAAGTAAGTATATAGTATATTAAGAAATGTTATGTAATTTGTTTGA 7872

Qy 351 AGGTCAATATCCTCAAAAACATTTGGAAATGTTCTGAGCTTGAAATAAACAATTGAGTGC 410
Db 7873 GAGAAATTTTGAATAAATGTTTTTTTATTAATGTTTGAAGTGTGG 7932
Qy 411 TTATTCAGATGACGATTAATTTATTTAGCTATATTTTTCTGTCAGAAATTCCTACT 470
Db 7933 TTTTATAGAAAGTAATAATTAATTAATGATTAAGATTAAGTGTGTTAATGAGCTTTTAA 7992
Qy 471 GGAGGAAATCAACATCAAAATGCCGCAAGATTTTAAATTAATGATTTCTATTTAC 530
Db 7993 ATAGTATTTT---AATTGAAATATGAATATGTTTAAATTAAGATTAATATTTGTT 8048
Qy 531 CTATCTGCTGTAACCTCACTGGAAGAGATTTTTCAAAAAATTTCATGAGAT 590
Db 8049 TAAAAATGTTTTCGTGATGTTTAAATGATTTTGAAGTTTAAATGAAATGTAT 8108
Qy 591 AGAGGCTAAATCATTAAGAAATTAATTT 618
Db 8109 AAATGTATATTAATTAAGATTAATTT 8136

RESULT 8

US-10-932-182A-166164/c

; Sequence 166164, Application US/10932182A

; GENERAL INFORMATION:

; APPLICANT: NAKAO, YOSHIHIRO

; APPLICANT: NAKAMURA, NORIHISA

; APPLICANT: KODAMA, YUKIKO

; APPLICANT: FUJIMURA, TOMOKO

; APPLICANT: ASHIKARI, TOSHIHIRO

; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS

; FILE REFERENCE: 030685-043

; CURRENT APPLICATION NUMBER: US/10/932,182A

; CURRENT FILING DATE: 2004-09-02

; NUMBER OF SEQ ID NOS: 197023

; SOFTWARE: Patent In version 3.3

; SEQ ID NO 166164

; LENGTH: 820

; TYPE: DNA

; ORGANISM: Saccharomyces pastorianus

; US-10-932-182A-166164

Query Match 4.0%; Score 40.2; DB 6; Length 820;
Best Local Similarity 41.8%; Pred. No. 2.2; Mismatches 338; Indels 0; Gaps 0;
Matches 243; Conservative 0;

Qy 70 ATAGTACGTATATCTAACTTAAGCAAAACAGATGAGGTCATACAGATCATATGGAAT 129
Db 594 ATAAATTAATCTTATACATATCATTTACAATATGTCATTTGCTTTTATTAATCTTTTACC 535
Qy 130 GAATATCGAGCTTAAGAAATTAATTAATGCTTAACGCTTGAGCTGAAGTATTCATAT 189
Db 534 CTATTAATTAATAAATAATTTCTAATAATTAATTAATTTCTTAATCCAAAGATTTAT 475
Qy 190 GTATCTAAACCTCCGATGACATTAATAAGATAAAGACGCTGAGAAATTTATCA 249
Db 474 ATATATATATATATATATATATATTTTAAATAAGATTAATTAATTAATTAATAA 415
Qy 250 GAATATATGCTTAATCTTCACTGACATCTGACATTAAGTGAATATGATCAATTTCTAAA 309
Db 414 ATTTATAGGCTTACTTCTGTTTAATTAATTAAGTGAATATTTAACTTAACTGCTCAAC 355
Qy 310 GATATGCAATATGTTTATTAAGATGATGATTTGAAGTCAATATCTCAAAAC 369
Db 354 TATATTAATTAAGATTAATTAAGATTAATGATTAATGATTAATTAATTAATTAATTA 295
Qy 370 ATTTGAATGTTCCGAGCTGAAATAAACAATGAAGTATTAATGATGATGAATAA 429
Db 294 TATATATTTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 235
Qy 430 TATATGACATATATTTTCTGTAAGAAATTTCACTGAGAAATCAACATCA 489


```
/ TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
/ FILE REFERENCE: 030685-043
/ CURRENT APPLICATION NUMBER: US/10/932,182A
/ CURRENT FILING DATE: 2004-09-02
/ NUMBER OF SEQ ID NOS: 197023
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 76518
/ LENGTH: 2460
/ TYPE: DNA
/ ORGANISM: Saccharomyces pastorianus
US-10-932-182A-76518

Query Match
Best Local Similarity 51.1%; Pred. No. 3.7;
Matches 93; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 134 ATCGAGCTAAGAAAATAATTTAGCTTACGCTTGGCTGAAGTGTATTCATTAAGTAT 193
DB 1475 ATATTAATATATATATATATATATATATATATATATATATATATATATATATATAT 1534
QY 194 CTAACTCTGATGACTATATTAAGAAATTAAGAGAGCTGAGAGATTTATCAAGAAAT 253
DB 1535 GATATGACGATATGACACCAACCAACCAACCAACCAACCAACCAACCAACCAACCAAC 1594
QY 254 ATATGCTATATCTTTGATCTGACATTAAGTGAAGAAATGCTGAATTTCTTAAGATA 313
DB 1595 ATGAATGTATTTCTACTTTTGTATACATCTGATGAAATATATGATGATGATGATGATA 1654
QY 314 TG 315
DB 1655 TG 1656

RESULT 12
US-10-517-441-414/C
/ Sequence 414, Application US/10517441
/ GENERAL INFORMATION:
/ APPLICANT: FOEKENS, John
/ APPLICANT: HARBESCK, Nadia
/ APPLICANT: KOENIG, Thomas
/ APPLICANT: MAIER, Sabine
/ APPLICANT: MARTENS, John
/ APPLICANT: MODEL, Fabian
/ APPLICANT: NIMMICH, Inko
/ APPLICANT: RUJAN, Tamas
/ APPLICANT: SCHMITT, Armin
/ APPLICANT: SCHMITT, Manfred
/ APPLICANT: LOOK, Maxime P.
/ APPLICANT: MARX, Almuth
/ APPLICANT: HOEFLE, Heinz
/ TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
/ TITLE OF INVENTION: proliferative disorders
/ FILE REFERENCE: 47675-93
/ CURRENT APPLICATION NUMBER: US/10/517,441
/ CURRENT FILING DATE: 2004-12-11
/ PRIOR APPLICATION NUMBER: PCT/EP2003/010881
/ PRIOR FILING DATE: 2003-10-01
/ PRIOR APPLICATION NUMBER: DE 10317955.0
/ PRIOR FILING DATE: 2003-04-17
/ PRIOR APPLICATION NUMBER: DE 10300096.8
/ PRIOR FILING DATE: 2003-01-07
/ PRIOR APPLICATION NUMBER: DE 10245779.4
/ PRIOR FILING DATE: 2002-10-01
/ NUMBER OF SEQ ID NOS: 2147
/ SEQ ID NO 414
/ LENGTH: 19634
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-414

Query Match 3.9%; Score 39.2; DB 7; Length 19634;
```

```
Best Local Similarity 44.7%; Pred. No. 6.5;
Matches 152; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 245 ATCAAGAAATATATGCTATCTTTGATCTGACATTAAGTGAAGAAATGATCAAAATTT 304
DB 10985 ATTAATCTTTATATATATATATATATATATATATATATATATATATATATATATAT 10926
QY 305 CTAAAGATATGCAAAATGTTTTATTAAGAAATGAATGAGATTTGAAGTCAATATCTTC 364
DB 10925 CTCTACAAAACCAAAATATTTCTTAATAATACCTTTATTTAACTCCATTTCTAAA 10866
QY 365 AAAACATTTGAAATGTTCTGAGCTTGAATAATCAATGAGTCTTATTCAGATGACG 424
DB 10865 TATATATATATATATATATATATATATATATATATATATATATATATATATAT 10806
QY 425 ATAAATTTATGACATATATTTTTTCTGTGACAGAAATTCACATGAGAGAAATCAAC 484
DB 10805 TTCAATATATATATATATATATATATATATATATATATATATATATATATATAT 10746
QY 485 ATCAAAATGCGCAAGATTTTAAATTAATTAATGATTTCTTAATTAACCTTATCTGTAA 544
DB 10745 TCTAAACCTATCAATTAATAATTAATAATTAATAATTAATAATTAATAATTAATAAT 10686
QY 545 CTTCACGTGGAAAGAGATTTTTCAAAAAATTTCACAA 584
DB 10685 ATATATATCAATCACTTAACTTTTAAATAATTAATATATATAA 10646

RESULT 13
US-10-517-441-688/C
/ Sequence 688, Application US/10517441
/ GENERAL INFORMATION:
/ APPLICANT: FOEKENS, John
/ APPLICANT: HARBESCK, Nadia
/ APPLICANT: KOENIG, Thomas
/ APPLICANT: MAIER, Sabine
/ APPLICANT: MARTENS, John
/ APPLICANT: MODEL, Fabian
/ APPLICANT: NIMMICH, Inko
/ APPLICANT: RUJAN, Tamas
/ APPLICANT: SCHMITT, Armin
/ APPLICANT: SCHMITT, Manfred
/ APPLICANT: LOOK, Maxime P.
/ APPLICANT: MARX, Almuth
/ APPLICANT: HOEFLE, Heinz
/ TITLE OF INVENTION: Method and nucleic acids for the improved treatment of breast cell
/ TITLE OF INVENTION: proliferative disorders
/ FILE REFERENCE: 47675-93
/ CURRENT APPLICATION NUMBER: US/10/517,441
/ CURRENT FILING DATE: 2004-12-11
/ PRIOR APPLICATION NUMBER: PCT/EP2003/010881
/ PRIOR FILING DATE: 2003-10-01
/ PRIOR APPLICATION NUMBER: DE 10317955.0
/ PRIOR FILING DATE: 2003-04-17
/ PRIOR APPLICATION NUMBER: DE 10300096.8
/ PRIOR FILING DATE: 2003-01-07
/ PRIOR APPLICATION NUMBER: DE 10245779.4
/ PRIOR FILING DATE: 2002-10-01
/ NUMBER OF SEQ ID NOS: 2147
/ SEQ ID NO 688
/ LENGTH: 19634
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
US-10-517-441-688

Query Match 3.9%; Score 39.2; DB 7; Length 19634;
Best Local Similarity 44.7%; Pred. No. 6.5;
Matches 152; Conservative 0; Mismatches 188; Indels 0; Gaps 0;

QY 245 ATCAAGAAATATATGCTATCTTTGATCTGACATTAAGTGAAGAAATGATCAAAATTT 304
DB 10985 ATTAATCTTTATATATATATATATATATATATATATATATATATATATATATATAT 10926
QY 305 CTAAAGATATGCAAAATGTTTTATTAAGAAATGAATGAGATTTGAAGTCAATATCTTC 364
DB 10925 CTCTACAAAACCAAAATATTTCTTAATAATACCTTTATTTAACTCCATTTCTAAA 10866
QY 365 AAAACATTTGAAATGTTCTGAGCTTGAATAATCAATGAGTCTTATTCAGATGACG 424
DB 10865 TATATATATATATATATATATATATATATATATATATATATATATATATATAT 10806
QY 425 ATAAATTTATGACATATATTTTTTCTGTGACAGAAATTCACATGAGAGAAATCAAC 484
DB 10805 TTCAATATATATATATATATATATATATATATATATATATATATATATATATAT 10746
QY 485 ATCAAAATGCGCAAGATTTTAAATTAATTAATGATTTCTTAATTAACCTTATCTGTAA 544
DB 10745 TCTAAACCTATCAATTAATAATTAATAATTAATAATTAATAATTAATAATTAATAAT 10686
QY 545 CTTCACGTGGAAAGAGATTTTTCAAAAAATTTCACAA 584
DB 10685 ATATATATCAATCACTTAACTTTTAAATAATTAATATATATAA 10646
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